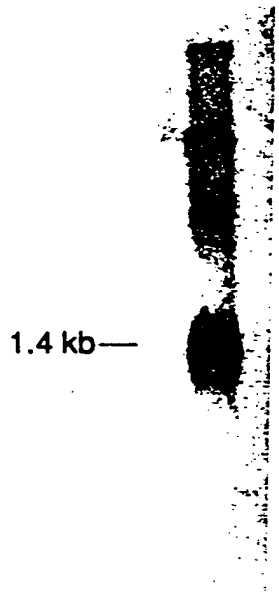

Figure 1

```
   1  CCCTTCTCCAGGGACTCTGGCTGCCAGCAGCTCCGCCTTTCAGATCAATTCTCGACCACC   60
                                                 M  L  P  V  C  H  R  F
  61  CACCTTGGGACTGCCGCCCAGTCCTGCCCTCTGGATCAGTGGGGTCCAGACACGCCCCCT  120
   C  D  H  L  L  L  L  L  L  L  P  S  T  T  L  A  P  A  P  A
 121  CCAGGACCTCAAAGCACCCCCGACCTAAGGTCACCAGCCCACTGGCCCCAGACGCAGTGG  180
   S  M  G  P  A  A  A  L  L  Q  V  L  G  L  P  E  A  P  R  S
 181  GCTCCGCTGACTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTT  240
   V  P  T  H  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P
 241  TTGCGACCACCTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGCGCCAGC  300
   Q  E  A  R  V  G  R  P  L  R  P  C  H  V  E  E  L  G  V  A
 301  ATCCATGGGCCCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCCGGAG  360
   G  N  I  V  R  H  I  P  D  S  G  L  S  S  R  P  A  Q  P  A
 361  CGTCCCCACACACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGTGACCC  420
   R  T  S  G  L  C  P  E  W  T  V  V  F  D  L  S  N  V  E  P
 421  CCAGGAGGCCAGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGGTCGC  480
   T  E  R  P  T  R  A  R  L  E  L  R  L  E  A  E  C  E  D  T
 481  CGGAAACATTGTGCGCCACATCCCCGACAGCGGTCTGTCCTCCAGGCCCGCACAACCCGC  540
                                                   could be Ser
   G  G  W  E  L  S  V  A  L  W  A  D  A  E  H  P  G  P  E  L
 541  CAGGACCTCGGGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTCGAATGTGGAGCC  600
   L  R  V  P  A  P  P  G  V  L  L  R  A  D  L  L  G  T  A  V
 601  CACAGAGCGCCCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGTGTGAAGATAC  660
   A  A  N  A  S  V  P  C  T  V  R  L  A  L  S  L  H  P  G  A
 661  AGGAGGGTGGGAGCTAAGCGTGGCACTGTGGGCCGACGCAGAGCATCCAGGGCCTGAGCT  720
   T  A  A  C  G  R  L  A  E  A  S  L  L  L  V  T  L  D  P  R
 721  GCTGCGCGTGCCGGCGCCACCAGGGGTGCTCCTGCGCGCAGACCTACTGGGGACTGCAGT  780
   L  C  P  L  P  R  L  R  R  H  T  E  P  R  V  E  V  G  P  V
 781  AGCCGCCAACGCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGC  840
   G  T  C  R  T  R  R  L  H  V  S  F  R  E  V  G  W  H  R  W
 841  CACTGCAGCCTGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACG  900
   V  I  A  P  R  G  F  L  A  N  F  C  Q  G  T  C  A  L  P  E
 901  CCTGTGTCCCTTGCCGCGATTGCGGCGCCACACGGAGCCCAGGGTAGAAGTTGGTCCAGT  960
   T  L  R  G  P  G  G  P  P  A  L  N  H  A  V  L  R  A  L  M
 961  GGGCACTTGTCGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTG 1020
   H  A  A  A  P  T  P  G  A  G  S  P  C  C  V  P  E  R  L  S
1021  GGTGATCGCGCCGCGTGGCTTCCTAGCCAACTTCTGCCAGGGCACGTGCGCACTACCCGA 1080
   P  I  S  V  L  F  F  D  N  S  D  N  V  V  L  R  H  Y  E  D
1081  AACGCTGAGGGGACCCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCAT 1140
   M  V  V  D  E  C  G  C  R
1141  GCACGCAGCTGCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATC 1200
1201  ACCCATCTCCGTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGA 1260
1261  CATGGTGGTGGATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCC 1320
1321  CCACGCAAAAGCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAA 1380
1381  TTTGACT  1387
```

```
GDF-1        RRHTEPRVEVG--PVGTCRTRRLHVSF-REVGWHRWVIAPRGFLANFCQGTCALPETLRGPGGPP

Vg-1         RKRSYSKLPFT--ASNICKKRHLYVEF-KDVGWQNWVIAPQGYMANYCYGECP-YPLTEILNG--
Vgr-1        GSGSSDYNGSE--LKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGEC-SFPLNAHMNA--
BMP-2a       KRQAKHKQRKR--LKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECP-FPLADHLNS--
BMP-2b       SPKHHSQRARK--KNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCP-FPLADHLNS--
BMP-3        TLKKARRKQWI--EPRNCARRYLKVDF-ADIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS--
DPP          -HARRPTRRKN--HDDTCRRHSLYVDF-SDVGWDDWIVAPLGYDAYYCHGKCP-FPLADHFNS--
MIS          GRAQRSAGATA--ADGPCALRELSVDLRAE----RSVLIPETYQANNCQGVCGWPQSDRNPRY--
Inhibin α    RLLQRPPEEPA--AHANCHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPV-
Inhibin βA   GLE---CDGKV---NICC-KKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL-
Inhibin βB   GLE---CDGRT---NLCC-RQQFFIDF-RLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSAS-
TGF-β1       ALDTNYCFSST--EKNCCVRQ-LYIDFRKDLGWK-WIHEPKGYHANFCLGPCP-YIW----SLD-
TGF-β2       ALDAAYCFRNV--QDNCCLRP-LYIDFKRDLGWK-WIHEPKGYNANFCAGACP-YLW----SSD-
TGF-β3       ALDTNYCFRNL--EENCCVRP-LYIDFRQDLGWK-WVHEPKGYYANFCSGPCP-YLR----SAD-
TGF-β4       DLDTDYCFGPGTDEKNCCVRP-LYIDFRKDLQWK-WIHEPKGYMANFCMGPCP-YIW----SAD-
TGF-β5       GVGQEYCFGNN--GPNCCVKP-LYINFRKDLGWK-WIHEPKGYEANYCLGNCP-YIW----SMD-


GDF-1        ALNHAVLRALMHAAA-PTPGAGSPCCV--PERLSPISVLFF-DNSDNVVLRHYEDMVVDECGCR

Vg-1         -SNHAILQTLVHS--IEPEDIPLPCCV--PTKMSPISMLFY-DNNDNVVLRHYENMAVDECGCR
Vgr-1        -TNHAIVQTLVHL--MNPEYVPKPCCA--PTKLNAISVLYF-DDNSNVILKKYRNMVVRACGCH
BMP-2a       -TNHAIVQTLVNS---VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR
BMP-2b       -TNHAIVQTLVNS---VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR
BMP-3        --NHATIQSIVRA-VGVVPGIPEPCCV--PEKMSSLSILFF-DENKNVVLKVYPNMTVESCACR
DPP          -TNHAVVQTLVNN--MNPGKVPKACCV--PTQLDSVAMLYLND-QSTVVLKNYQEMTVVGCGCR
MIS          -GNH-VVLLL-KMQARGAALARPPCCV--PTAYAGKLLISLSEER--ISAHHVPNMVATECGCR
Inhibin α    -PGAPPT----PAQPYSLLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
Inhibin βA   -SFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYY-DDGQNIIKKDIQNMIVEECGCS
Inhibin βB   -SFHTAVVNQYRMRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA
TGF-β1       -TQYSKVLALYN--QHNPGASAAPCCV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS
TGF-β2       -TQHSRVLSLYN--TINPEASASPCCV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCKCS
TGF-β3       -TTHSTVLGLYN--TLNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSCKCS
TGF-β4       -TQYTKVLALYN--QHNPGASAAPCCV--PQTLDPLPIIYY-VGRNVRV-EQLSNMVVRACKCS
TGF-β5       -TQYSKVLSLYN--QNNPGASISPCCV--PDVLEPLPIIYY-VGRTAKV-EQLSNMVVRSCNCS
```

07/614452
08/090002

Figure 3a

	GDF-1	Vg-1	Vgr-1	BMP-2a	BMP-2b	BMP-3	DPP	MIS	Inhibin α	Inhibin βA	Inhibin βB	TGF-β1	TGF-β2	TGF-β3	TGF-β4	TGF-β5
GDF-1	100	52	40	38	39	41	34	33	22	31	31	26	27	30	26	26
Vg-1	–	100	59	59	57	45	49	27	23	45	40	34	35	38	33	35
Vgr-1	–	–	100	62	59	43	57	26	23	45	39	35	37	38	37	37
BMP-2a	–	–	–	100	92	44	73	26	20	42	37	34	34	35	33	33
BMP-2b	–	–	–	–	100	44	74	27	21	41	37	33	34	35	33	33
BMP-3	–	–	–	–	–	100	42	25	28	33	33	29	31	31	26	28
DPP	–	–	–	–	–	–	100	25	20	39	36	35	35	35	35	34
MIS	–	–	–	–	–	–	–	100	18	22	22	24	21	26	25	24
Inhibin α	–	–	–	–	–	–	–	–	100	23	21	24	23	24	24	24
Inhibin βA	–	–	–	–	–	–	–	–	–	100	63	38	37	36	35	38
Inhibin βB	–	–	–	–	–	–	–	–	–	–	100	35	35	36	34	32
TGF-β1	–	–	–	–	–	–	–	–	–	–	–	100	73	77	85	81
TGF-β2	–	–	–	–	–	–	–	–	–	–	–	–	100	81	68	69
TGF-β3	–	–	–	–	–	–	–	–	–	–	–	–	–	100	74	73
TGF-β4	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	78
TGF-β5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100

Figure 3b

```
                                                                                                  133
         54
GDF-1     PVPPVMWRLFRRRDPQEARVGRPLRPCHVEELGVAGNIVRHIPDSGLSSRPAQPARTSGLCPEWTVVFDLSNVEPTERPT
          |||   || |  |          |   | |||  | |   |  || |    |          | |    |  |  |  || |
Vg-1      PVPSILWRIFNQRMGSSIQKKKPDL CFVEEFNVPGSVIRVFPDQGRFIIPYSDDIHPTQCLEKRLFFNISAIEKEERVT
                                                                                          124
         46
```

```
         219               234
GDF-1      SLLLVTLDPRLCPLPR
           ||| ||| |  |  ||
Vg-1       SLLTVTLNPLRCKRPR
         228               243
```

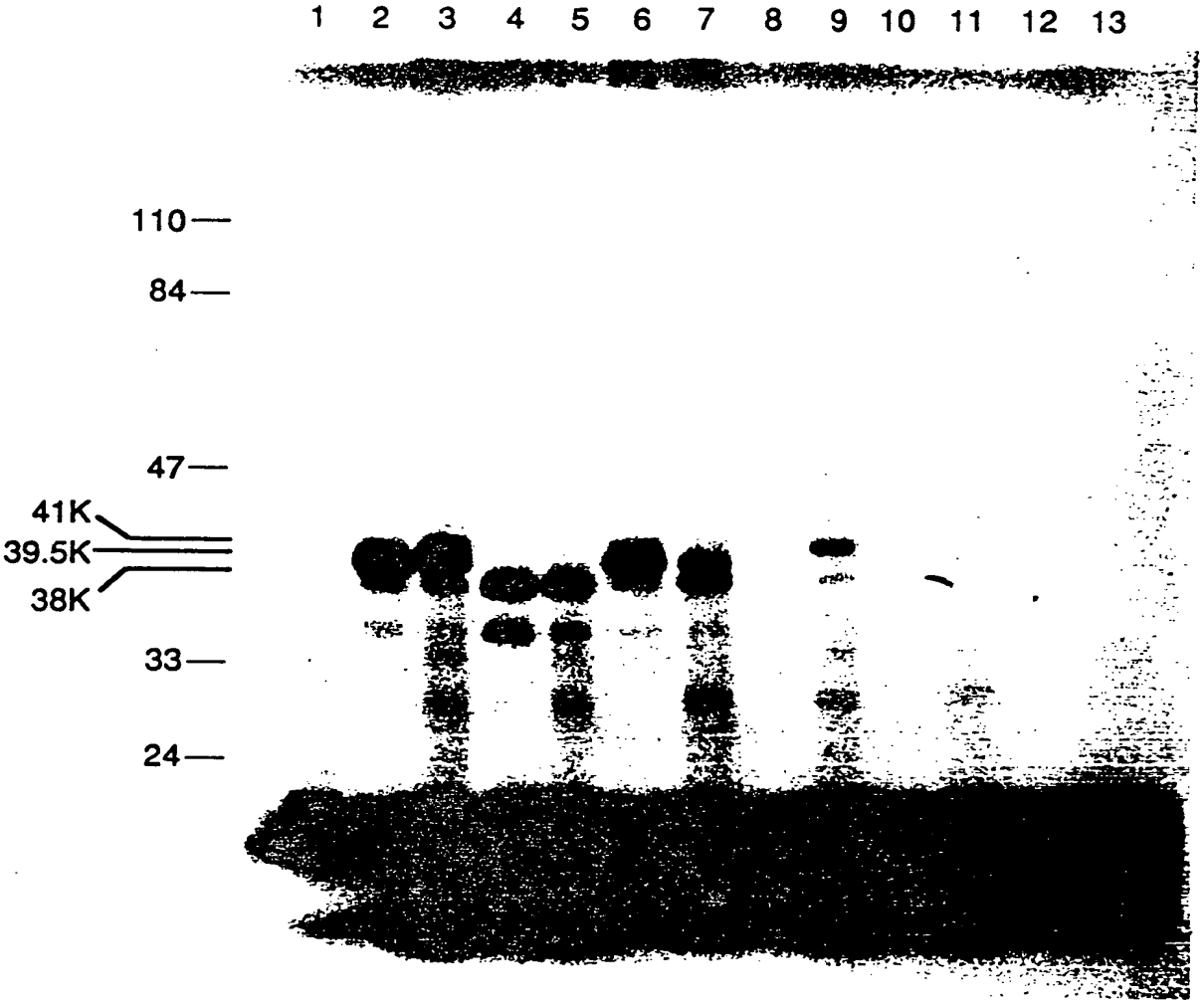

Figure 4

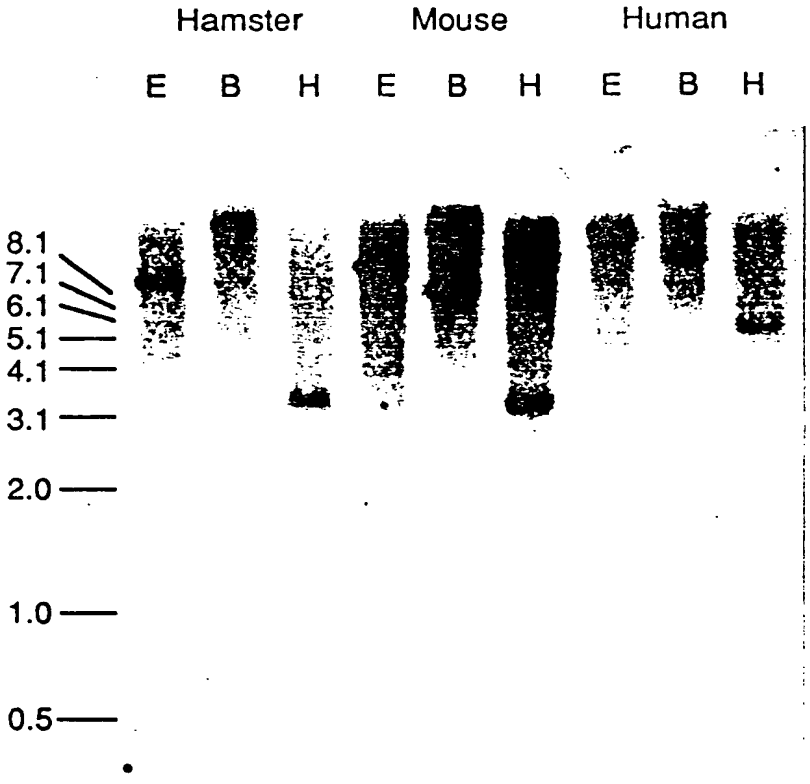

Figure 5

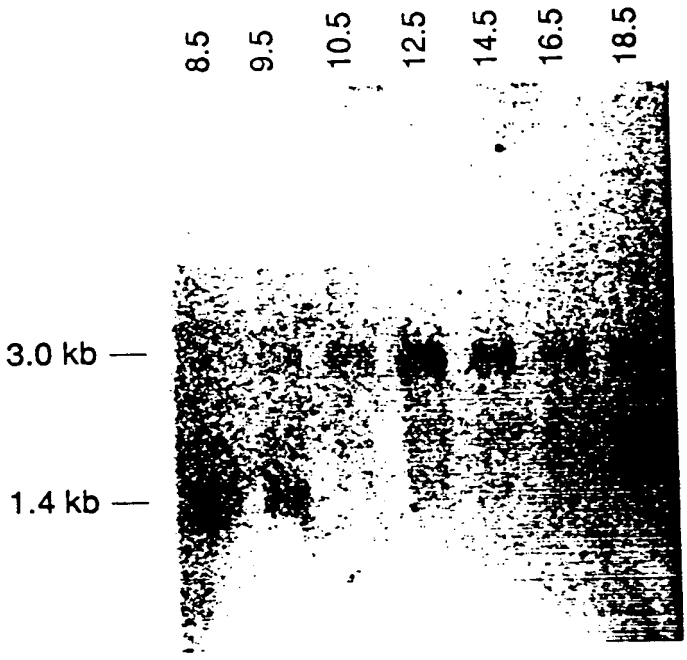

Figure 6

07 614452
08/090002

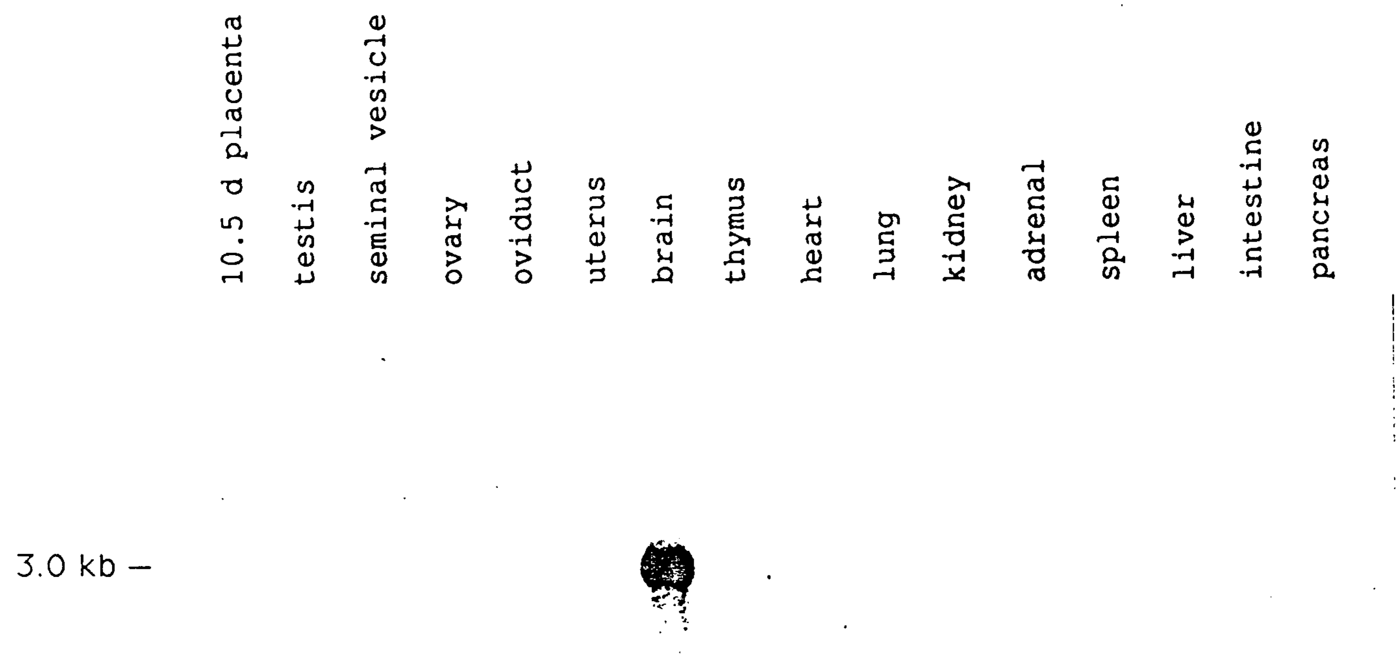

Figure 7

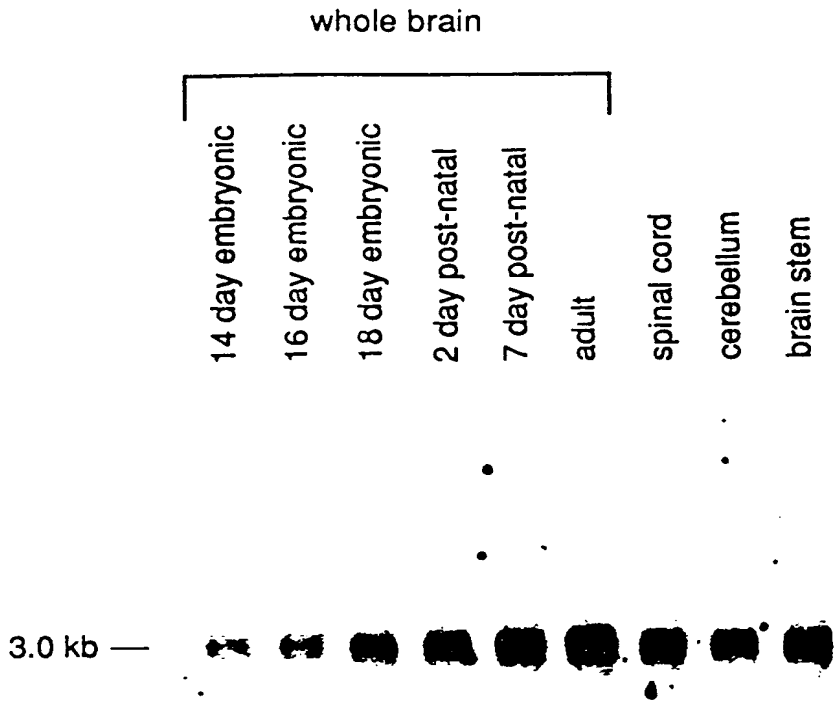

Figure 8

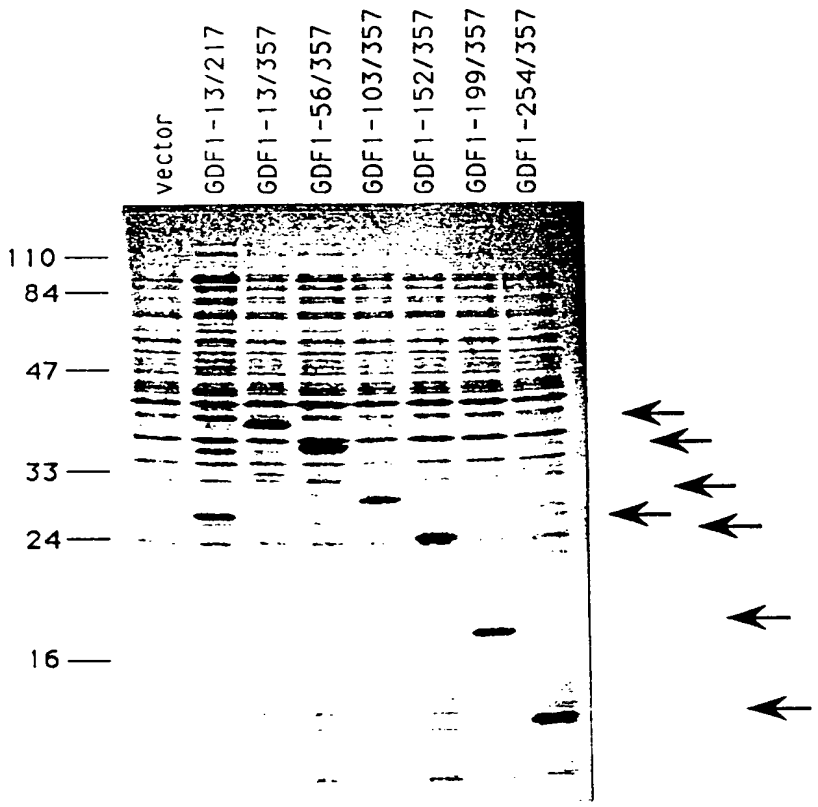

Figure 9

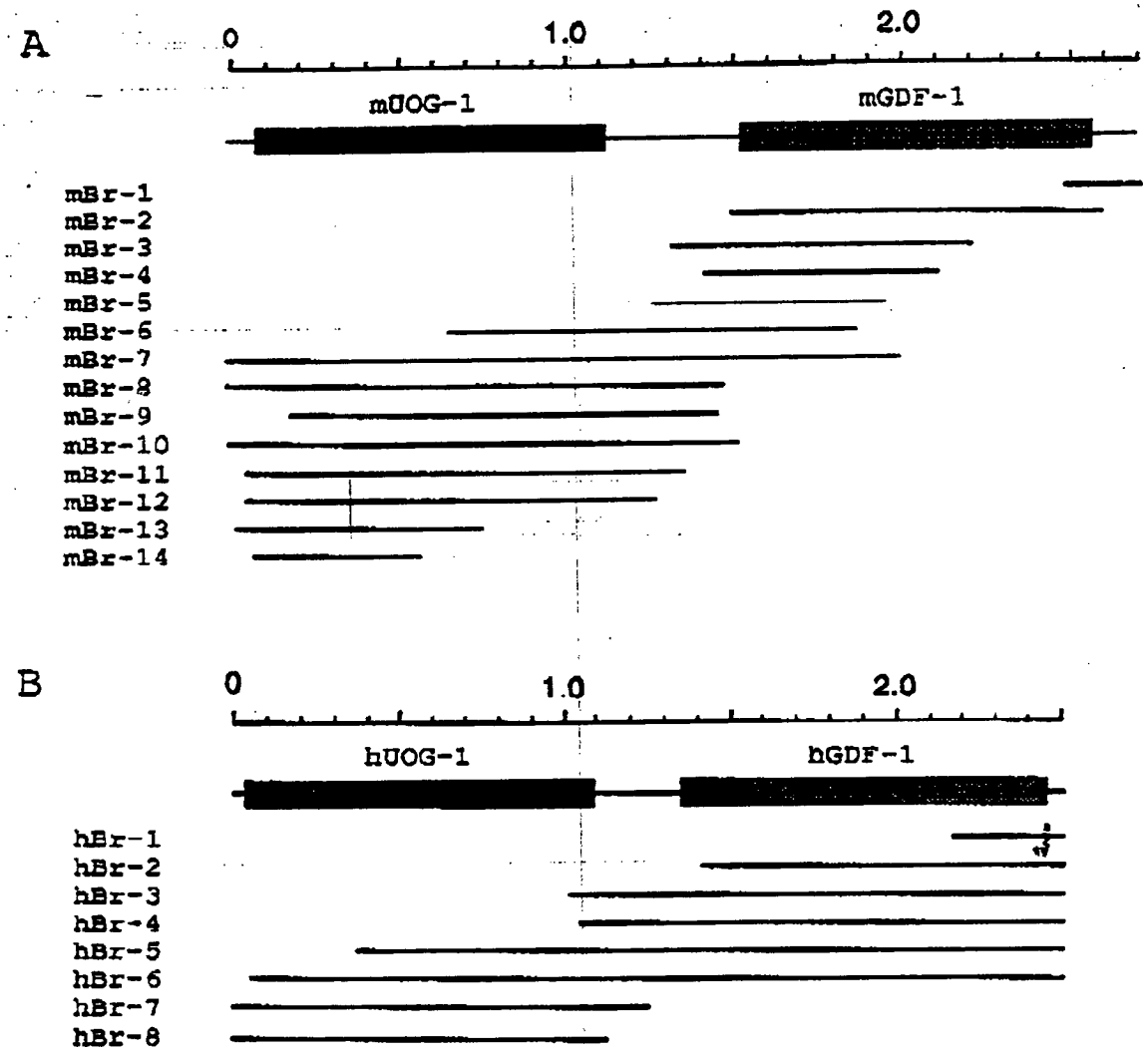
A
0
1.0
2.0
mUOG-1
mGDF-1
mBr-1
mBr-2
mBr-3
mBr-4
mBr-5
mBr-6
mBr-7
mBr-8
mBr-9
mBr-10
mBr-11
mBr-12
mBr-13
mBr-14
B
0
1.0
2.0
hUOG-1
hGDF-1
hBr-1
hBr-2
hBr-3
hBr-4
hBr-5
hBr-6
hBr-7
hBr-8

Figure 10

```
1     GCGCGTGACGCGAGGGCGCGCGGCGACTCGGACCGGTGCAGGCAACAGCGGAGACAGCGG   60
61    AGAATTGGATAGCATGGCTGCTGCCGCGGCGACCCCCAGGCTCGAGGCGCCAGAGCCCAT  120
                 M  A  A  A  A  A  T  P  R  L  E  A  P  E  P  M
121   GCCGAGTTATGCGCAGATGTTGCAACGAAGCTGGGCCTCGGCGCTGGCGGCGGCTCAGGG  180
      P  S  Y  A  Q  M  L  Q  R  S  W  A  S  A  L  A  A  A  Q  G
181   CTGCGGGGACTGCGGCTGGGGACTGGCGCGCCGCGGCCTGGCGGAGCACGCGCACCTGGC  240
      C  G  D  C  G  W  G  L  A  R  R  G  L  A  E  H  A  H  L  A
241   TGCACCCGAGCTGCTGCTGGCCGTGCTCTGCGCTCTGGGGTGGACAGCGTTGCGCTGGGC  300
      A  P  E  L  L  L  A  V  L  C  A  L  G  W  T  A  L  R  W  A
301   AGCCACCACACACATCTTTCGGCCCCTGGCCAAGCGGTGTCGTCTGCAGCCTAGAGATGC  360
      A  T  T  H  I  F  R  P  L  A  K  R  C  R  L  Q  P  R  D  A
361   TGCCAGGTTACCTGAGAGCGCCTGGAAGCTTCTGTTCTACTTGGCCTGTTGGAGCTACTG  420
      A  R  L  P  E  S  A  W  K  L  L  F  Y  L  A  C  W  S  Y  C
421   CGCTTACCTGCTCCTGGGCACCAGTTATCCTTTCTTCCATGACCCGCCCTCTGTCTTCTA  480
      A  Y  L  L  L  G  T  S  Y  P  F  F  H  D  P  P  S  V  F  Y
481   TGACTGGAGGTCAGGCATGGCAGTGCCCTGGGACATCGCGGTGGCCTATTTGCTGCAGGG  540
      D  W  R  S  G  M  A  V  P  W  D  I  A  V  A  Y  L  L  Q  G
541   GAGTTTCTACTGCCACTCCATCTATGCCACCGTGTACATGGACAGCTGGCGTAAGGACTC  600
      S  F  Y  C  H  S  I  Y  A  T  V  Y  M  D  S  W  R  K  D  S
601   GGTGGTCATGCTGGTGCATCACGTGGTCACCCTGCTCCTCATTGCCTCTTCCTACGCCTT  660
      V  V  M  L  V  H  H  V  V  T  L  L  L  I  A  S  S  Y  A  F
661   CCGGTACCACAACGTAGGCCTCCTCGTGTTCTTCCTGCATGACGTCAGCGATGTGCAGCT  720
      R  Y  H  N  V  G  L  L  V  F  F  L  H  D  V  S  D  V  Q  L
721   GGAGTTCACAAAACTCAACATCTACTTTAAGGCTAGGGGTGGTGCCTACCATCGCTTGCA  780
      E  F  T  K  L  N  I  Y  F  K  A  R  G  G  A  Y  H  R  L  H
781   TGGGCTGGTGGCCAACCTGGGCTGCCTCAGCTTCTGTTTCTGCTGGTTCTGGTTCCGCCT  840
      G  L  V  A  N  L  G  C  L  S  F  C  F  C  W  F  W  F  R  L
841   CTACTGGTTCCCGCTCAAGGTTCTGTACGCCACTTGCCACTGCAGCCTGCAGTCTGTGCC  900
      Y  W  F  P  L  K  V  L  Y  A  T  C  H  C  S  L  Q  S  V  P
901   TGACATTCCGTACTACTTCTTCTTCAACATTCTGCTGTTGCTCCTGATGGTCATGAACAT  960
      D  I  P  Y  Y  F  F  F  N  I  L  L  L  L  M  V  M  N  I
961   CTATTGGTTCCTGTACATTGTGGCTTTCGCAGCCAAGGTGCTGACTGGTCAGATGCGTGA 1020
      Y  W  F  L  Y  I  V  A  F  A  A  K  V  L  T  G  Q  M  R  E
1021  ACTGGAAGACTTGAGGGAGTACGACACTCTGGAAGCTCAGACAGCCAAGCCCTGCAAAGC 1080
      L  E  D  L  R  E  Y  D  T  L  E  A  Q  T  A  K  P  C  K  A
1081  CGAGAAGCCACTGAGGAATGGCCTGGTGAAGGACAAGCTCTTCTGAGTCTCTTGTCCTCA 1140
      E  K  P  L  R  N  G  L  V  K  D  K  L  F
1141  ACTTCAGCCATCCAGGACTCTATCCCATCCTACCTGGGATACTGACTCCGCCCCTGGAGA  1200
1201  CTCGACCCAGTCCCTGGAGGTCTGCTCCCACCCCTGGAGGCCCGGTCCCGCCTTTGGCGG  1260
1261  CATGGCCTCGCCCCTAGGACAATAGCCCCGCCCTAAGATTCAGGATGCTACCCTTCTCCA  1320
1321  GGGACTCTGGCTGCCAGCAGCTCCGCCTTTCAGATCAATTCTCGACCACCCACCTTGGGA  1380
1381  CTGCCGCCCAGTCCTGCCCTCTGGATCAGTGGGGTCCAGACACGCCCCCTCCAGGACCTC  1440
1441  AAAGCACCCCCGACCTAAGGTCACCAGCCCACTGGCCCCAGACGCAGTGGGCTCCGCTGA  1500
1501  CTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTTTTGCGACCAC  1560
                                  M  L  P  V  C  H  R  F  C  D  H
1561  CTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGCGCCAGCATCCATGGGC  1620
      L  L  L  L  L  L  L  P  S  T  T  L  A  P  A  P  A  S  M  G
1621  CCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCCGGAGCGTCCCCACA  1680
      P  A  A  A  L  L  Q  V  L  G  L  P  E  A  P  R  S  V  P  T
1681  CACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGCGACCCCCAGGAGGCC  1740
      H  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P  Q  E  A
1741  AGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGGTCGCCGGAAACATT  1800
      R  V  G  R  P  L  R  P  C  H  V  E  E  L  G  V  A  G  N  I
1801  GTGCGCCACATCCCCGACAGCGGTCTGTCCTCCAGGCCCGCACAACCCGCCAGGACCTCG  1860
      V  R  H  I  P  D  S  G  L  S  S  R  P  A  Q  P  A  R  T  S
1861  GGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTCGAATGTGGAGCCCACAGAGCGC  1920
      G  L  C  P  E  W  T  V  V  F  D  L  S  N  V  E  P  T  E  R
1921  CCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGAGTGAAGATACAGGGGGGTGG  1980
      P  T  R  A  R  L  E  L  R  L  E  A  E  S  E  D  T  G  G  W
1981  GAGCTAAGCGTGGCACTGTGGGCCGACGCAGAGCATCCAGGGCCTGAGCTGCTGCGCGTG  2040
      E  L  S  V  A  L  W  A  D  A  E  H  P  G  P  E  L  L  R  V
2041  CCGGCGCCACCAGGGGTGCTCCTGCGCGCAGACCTACTGGGGACTGCAGTAGCCGCCAAC  2100
      P  A  P  P  G  V  L  L  R  A  D  L  L  G  T  A  V  A  A  N
2101  GCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGCCACTGCAGCC  2160
      A  S  V  P  C  T  V  R  L  A  L  S  L  H  P  G  A  T  A  A
2161  TGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACGCCTGTGTCCC  2220
      C  G  R  L  A  E  A  S  L  L  L  V  T  L  D  P  R  L  C  P
2221  TTGCCGCGATTGCGGCGCCACACGGAGCCCAGGGTAGAAGTTGGTCCAGTGGGCACTTGT  2280
      L  P  R  L  R  R  H  T  E  P  R  V  E  V  G  P  V  G  T  C
2281  CGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTGGGTGATCGCG  2340
      R  T  R  R  L  H  V  S  F  R  E  V  G  W  H  R  W  V  I  A
2341  CCGCGTGGCTTCCTAGCCAACTTCTGCCAGGGCACGTGCGCACTACCCGAAACGCTGAGG  2400
      P  R  G  F  L  A  N  F  C  Q  G  T  C  A  L  P  E  T  L  R
2401  GGACCCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCAGCT  2460
      G  P  G  G  P  P  A  L  N  H  A  V  L  R  A  L  M  H  A  A
2461  GCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATCACCCATCTCC  2520
      A  P  T  P  G  A  G  S  P  C  C  V  P  E  R  L  S  P  I  S
2521  GTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGACATGGTGGTG  2580
      V  L  F  F  D  N  S  D  N  V  V  L  R  H  Y  E  D  M  V  V
2581  GATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCCCCACGCAAAA  2640
      D  E  C  G  C  R
2641  GCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAATTTGACTAAA  2700
2701  AATTAAGTTCC  2711
```

Fig 11A

murine

could be cys

~~07 614452~~
08/09 0002

```
1     GGACACGGCGGGCGAGCGGGCGGTATGGCGGCGGCGGGGCCCGCGGCGGGGCCGACGGGG   60
                                M  A  A  A  G  P  A  A  G  P  T  G
61    CCCGAGCCCATGCCGAGCTACGCGCAGCTAGTGCAGCGCGGCTGGGGCAGCGCGCTGGCG  120
      P  E  P  M  P  S  Y  A  Q  L  V  Q  R  G  W  G  S  A  L  A
121   GCGGCGCGGGGCTGCACGGACTGCGGCTGGGGGCTGGCGCGTCGCGGCCTGGCTGAGCAC  180
      A  A  R  G  C  T  D  C  G  W  G  L  A  R  R  G  L  A  E  H
181   GCGCACCTGGCGCCGCCCGAGCTGCTGCTGCTGGCGCTCGGCGCGCTGGGCTGGACCGCG  240
      A  H  L  A  P  P  E  L  L  L  L  A  L  G  A  L  G  W  T  A
241   CTGCGCTCCGCGGCCACTGCGCGCCTCTTTCGGCCCCTGGCGAAGCGGTGCTGCCTCCAG  300
      L  R  S  A  A  T  A  R  L  F  R  P  L  A  K  R  C  C  L  Q
301   CCCAGAGATGCCGCCAAGATGCCCGAGAGCGCTTGGAAGTTTCTCTTCTACCTGGGCAGC  360
      P  R  D  A  A  K  M  P  E  S  A  W  K  F  L  F  Y  L  G  S
361   TGGAGCTACAGTGCCTACCTGCTGTTTGGCACCGACTACCCCTTCTTCCATGACCCACCA  420
      W  S  Y  S  A  Y  L  L  F  G  T  D  Y  P  F  F  H  D  P  P
421   TCTGTCTTCTACGACTGGACGCCGGGCATGGCAGTGCCACGGGACATTGCAGCCGCCTAC  480
      S  V  F  Y  D  W  T  P  G  M  A  V  P  R  D  I  A  A  A  Y
481   CTGCTCCAGGGAAGCTTCTATGGCCACTCCATCTACGCTACGCTATACATGGACACCTGG  540
      L  L  Q  G  S  F  Y  G  H  S  I  Y  A  T  L  Y  M  D  T  W
541   CGCAAGGACTCGGTGGTCATGCTGCTCCACCACGTGGTCACTCTCATCCTCATCGTCTCC  600
      R  K  D  S  V  V  M  L  L  H  H  V  V  T  L  I  L  I  V  S
601   TCCTACGCCTTCCGGTACCACAATGTGGGCATCCTTGTGCTCTTCCTGCACGATATCAGT  660
      S  Y  A  F  R  Y  H  N  V  G  I  L  V  L  F  L  H  D  I  S
661   GACGTGCAGCTTGAGTTCACCAAGCTCAACATTTACTTCAAGTCCCGCGGCGGCTCCTAC  720
      D  V  Q  L  E  F  T  K  L  N  I  Y  F  K  S  R  G  G  S  Y
721   CATCGGCTGCATGCCTTGGCAGCAGACTTGGGCTGCCTCAGCTTCGGCTTCAGCTGGTTC  780
      H  R  L  H  A  L  A  A  D  L  G  C  L  S  F  G  F  S  W  F
781   TGGTTCCGCCTCTACTGGTTCCCGCTCAAGGTCCTGTATGCCACCAGTCACTGCAGTCTG  840
      W  F  R  L  Y  W  F  P  L  K  V  L  Y  A  T  S  H  C  S  L
841   CGCACGGTGCCTGACATCCCCTTCTACTTCTTCTTCAATGCGCTCCTGCTGCTGCTCACC  900
      R  T  V  P  D  I  P  F  Y  F  F  F  N  A  L  L  L  L  L  T
901   CTTATGAACCTCTACTGGTTCCTGTACATCGTGGCGTTTGCAGCCAAGGTGTTGACAGGC  960
      L  M  N  L  Y  W  F  L  Y  I  V  A  F  A  A  K  V  L  T  G
961   CAGGTGCACGAGCTGAAGGACCTGCGGGAGTATGACACAGCCGAGGCCCAGAGCCTGAAG 1020
      Q  V  H  E  L  K  D  L  R  E  Y  D  T  A  E  A  Q  S  L  K
1021  CCCAGCAAAGCCGAGAAGCCACTGAGGAACGGCCTGGTGAAGGACAAGCGCTTCTGAACC 1080
      P  S  K  A  E  K  P  L  R  N  G  L  V  K  D  K  R  F
1081  CCTCGGCCCCGCCCCCGTGGACCCGGCCCCACCCCGAATACCCCGGCCACGCTCCCCGTC 1140
1141  CTTGGCCGCCCCTCCACCCCCTCCAACTCTGCTCCTCTAGGGCCGCCGCCACCTCCCCTG 1200
1201  GGACCCCGCCCCCTCATCCTGCCTCCATTTCCCGGCCACGCCCCCCAGGACCCCTGCCCC 1260
1261  TCCGGGGACACCGGCCCCGCCCTCAGCCCACTGGTCCCGGGCCGCCGCGGACCCTGCGCA 1320
1321  CTCTCTGGTCATCGCCTGGGAGGAAGATGCCACCGCCGCAGCAAGGTCCCTGCGGCCACC 1380
                                M  P  P  P  Q  Q  G  P  C  G  H  H
1381  ACCTCCTCCTCCTCCTGGCCCTGCTGCTGCCCTCGCTGCCCCTGACCCGCGCCCCCGTGC 1440
        L  L  L  L  L  A  L  L  L  P  S  L  P  L  T  R  A  P  V  P
1441  CCCCAGGCCCAGCCGCCGCCCTGCTCCAGGCTCTAGGACTGCGCGATGAGCCCCAGGGTG 1500
        P  G  P  A  A  A  L  L  Q  A  L  G  L  R  D  E  P  Q  G  A
1501  CCCCCAGGCTCCGGCCGGTTCCCCCGGTCATGTGGCGCCTGTTTCGACGCCGGGACCCCC 1560
        P  R  L  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P  Q
1561  AGGAGACCAGGTCTGGCTCGCGGCGGACGTCCCCAGGGGTCACCCTGCAACCGTGCCACG 1620
        E  T  R  S  G  S  R  R  T  S  P  G  V  T  L  Q  P  C  H  V
1621  TGGAGGAGCTGGGGGTCGCCGGAAACATCGTGCGCCACATCCCGGACCGCGGTGCGCCCA 1680
        E  E  L  G  V  A  G  N  I  V  R  H  I  P  D  R  G  A  P  T
1681  CCCGGGCCTCGGAGCCTGTCTCGGCCGCGGGGCATTGCCCTGAGTGGACAGTCGTCTTCG 1740
        R  A  S  E  P  V  S  A  A  G  H  C  P  E  W  T  V  V  F  D
1741  ACCTGTCGGCTGTGGAACCCGCTGAGCGCCCGAGCCGGGCCCGCCTGGAGCTGCGTTTCG 1800
        L  S  A  V  E  P  A  E  R  P  S  R  A  R  L  E  L  R  F  A
1801  CGGCGGCGGCGGCGGCAGCCCCGGAGGGCGGCTGGGAGCTGAGCGTGGCGCAAGCGGGCC 1860
        A  A  A  A  A  A  P  E  G  G  W  E  L  S  V  A  Q  A  G  Q
1861  AGGGCGCGGGCGCGGACCCCGGGCCGGTGCTGCTCCGCCAGTTGGTGCCCGCCCTGGGGC 1920
        G  A  G  A  D  P  G  P  V  L  L  R  Q  L  V  P  A  L  G  P
1921  CGCCAGTGCGCGCGGAGCTGCTGGGCGCCGCTTGGGCTCGCAACGCCTCATGGCCGCGCA 1980
        P  V  R  A  E  L  L  G  A  A  W  A  R  N  A  S  W  P  R  S
1981  GCCTCCGCCTGGCGCTGGCGCTACGCCCCCGGGCCCCTGCCGCCTGCGCGCGCCTGGCCG 2040
        L  R  L  A  L  A  L  R  P  R  A  P  A  A  C  A  R  L  A  E
2041  AGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCCCGGCCGC 2100
        A  S  L  L  L  V  T  L  D  P  R  L  C  H  P  L  A  R  P  R
2101  GGCGCGACGCCGAACCCGTGTTGGGCGGCGGCCCCGGGGGCGCTTGTCGCGCGCGGCGGC 2160
        R  D  A  E  P  V  L  G  G  G  P  G  G  A  C  R  A  R  R  L
2161  TGTACGTGAGCTTCCGCGAGGTGGGCTGGCACCGCTGGGTCATCGCGCCGCGCGGCTTCC 2220
        Y  V  S  F  R  E  V  G  W  H  R  W  V  I  A  P  R  G  F  L
2221  TGGCCAACTACTGCCAGGGTCAGTGCGCGCTGCCCGTCGCGCTGTCGGGGTCCGGGGGGC 2280
        A  N  Y  C  Q  G  Q  C  A  L  P  V  A  L  S  G  S  G  G  P
2281  CGCCGGCGCTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCGGCCGCCCCGGGAGCCG 2340
        P  A  L  N  H  A  V  L  R  A  L  M  H  A  A  A  P  G  A  A
2341  CCGACCTGCCCTGCTGCGTGCCCGCGCGCCTGTCGCCCATCTCCGTGCTCTTCTTTGACA 2400
        D  L  P  C  C  V  P  A  R  L  S  P  I  S  V  L  F  F  D  N
2401  ACAGCGACAACGTGGTGCTGCGGCAGTATGAGGACATGGTGGTGGACGAGTGCGGCTGCC 2460
        S  D  N  V  V  L  R  Q  Y  E  D  M  V  V  D  E  C  G  C  R
2461  GCTAACCCGGGGCGGGCAGGGACGCGGGCCCAACAATAAATGCCGCGTGG  2510
```

Fig 11B

human

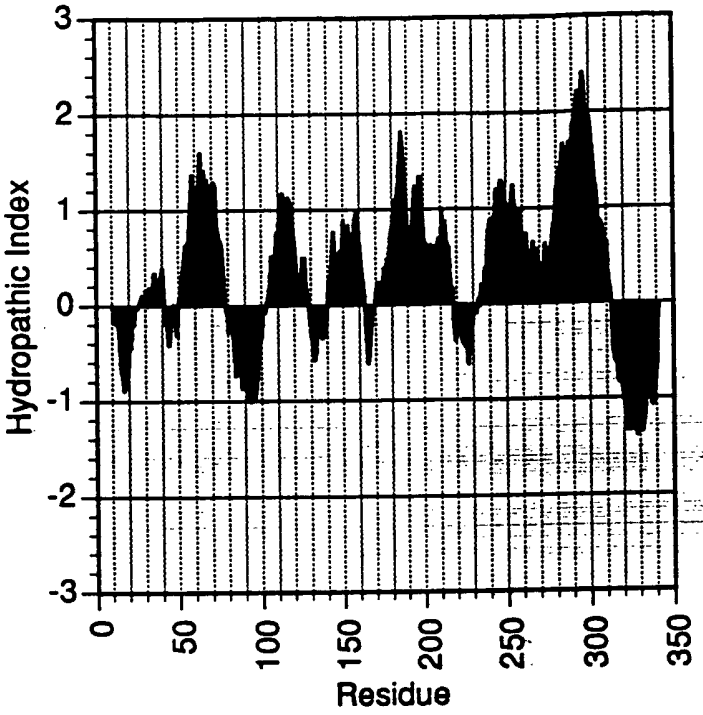

Fig 12

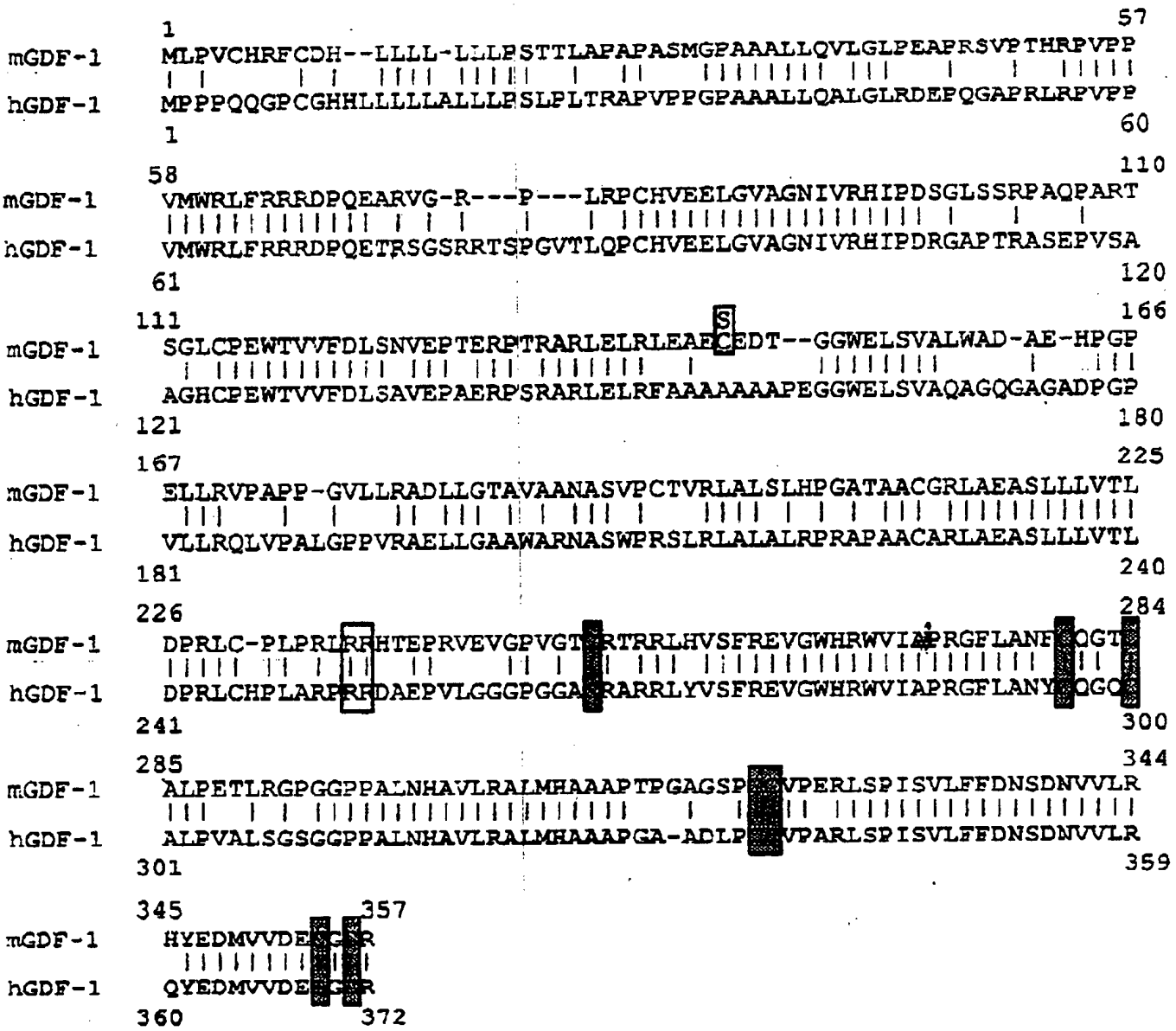
1 57
mGDF-1 MLPVCHRFCDH--LLLL-LLLPSTTLAPAPASMGPAAALLQVLGLPEAPRSVPTHRPVPP
hGDF-1 MPPPQQGPCGHHLLLLLALLLPSLPLTRAPVPPGPAAALLQALGLRDEPQGAPRLRPVPP
1 60
58 110
mGDF-1 VMWRLFRRRDPQEARVG-R---P---LRPCHVEELGVAGNIVRHIPDSGLSSRPAQPART
hGDF-1 VMWRLFRRRDPQETRSGSRRTSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPVSA
61 120
111 166
mGDF-1 SGLCPEWTVVFDLSNVEPTERPTRARLELRLEAPCEDT--GGWELSVALWAD-AE-HPGP
hGDF-1 AGHCPEWTVVFDLSAVEPAERPSRARLELRFAAAAAAAPEGGWELSVAQAGQGAGADPGP
121 180
167 225
mGDF-1 ELLRVPAPP-GVLLRADLLGTAVAANASVPCTVRLALSLHPGATAACGRLAEASLLLVTL
hGDF-1 VLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASLLLVTL
181 240
226 284
mGDF-1 DPRLC-PLPRLRRHTEPRVEVGPVGTGRTRRLHVSFREVGWHRWVIAPRGFLANFYQGT
hGDF-1 DPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYAQGQ
241 300
285 344
mGDF-1 ALPETLRGPGGPPALNHAVLRALMHAAAPTPGAGSPCVPERLSPISVLFFDNSDNVVLR
hGDF-1 ALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPCVPARLSPISVLFFDNSDNVVLR
301 359
345 357
mGDF-1 HYEDMVVDECGCR
hGDF-1 QYEDMVVDECGCR
360 372

Fig 8a

```
                1                                                          60
mUOG-1          MAAAAATPRLEAPEPMPSYAQMLQRSWASALAAAQGCGDCGWGLARRGLAEHAHLAAPEL
                |||| |||||||||  || | |:|||| || ||||||||||||||||||| |||
hUOG-1          MAAAGPAAGPTGPEPMPSYAQLVQRGWGSALAAARGCTDCGWGLARRGLAEHAHLAPPEL
                1                                                          60

               61                                                         120
mUOG-1          LLAVLCALGWTALRWAATTHIFRPLAKRCRLQPRDAARLPESAWKLLFYLACWSYCAYLL
                ||  | |||||||| ||| |||||||| ||||||| |||||| |||| ||| ||||
hUOG-1          LLLALGALGWTALRSAATARLFRPLAKRCCLQPRDAAKMPESAWKFLFYLGSWSYSAYLL
               61                                                         120

              121                                                         180
mUOG-1          LGTSYPFFHDPPSVFYDWRSGMAVPWDIAVAYLLQGSFYCHSIYATVYMDSWRKDSVVML
                || |||||||||||||| ||||| ||| ||||||||| ||||||| ||| |||||||||
hUOG-1          FGTDYPFFHDPPSVFYDWTPGMAVPRDIAAAYLLQGSFYGHSIYATLYMDTWRKDSVVML
              121                                                         180

              181                                                         240
mUOG-1          VHHVVTLLLIASSYAFRYHNVGLLVFFLHDVSDVQLEFTKLNIYFKARGGAYHRLHGLVA
                |||||| || |||||||||| || |||| |||||||||||||| ||| ||||| | |
hUOG-1          LHHVVTLILIVSSYAFRYHNVGILVLFLHDISDVQLEFTKLNIYFKSRGGSYHRLHALAA
              181                                                         240

              241                                                         300
mUOG-1          NLGCLSFCFCWFWFRLYWFPLKVLYATCHCSLQSVPDIPYYFFFNILLLLLMVMNIYWFL
                |||||| | ||||||||||||||||| |||| ||||| ||||| ||||| |||||||
hUOG-1          DLGCLSFGFSWFWFRLYWFPLKVLYATSHCSLRTVPDIPFYFFFNALLLLLTLMNLYWFL
              241                                                         300

              301                                                  350
mUOG-1          YIVAFAAKVLTGQMRELEDLREYDTLEAQTAKPCKAEKPLRNGLVKDKLF
                |||||||||||||| || ||||||| ||| || ||||||||||||| |
hUOG-1          YIVAFAAKVLTGQVHELKDLREYDTAEAQSLKPSKAEKPLRNGLVKDKRF
              301                                                  350
```

Fig 13b

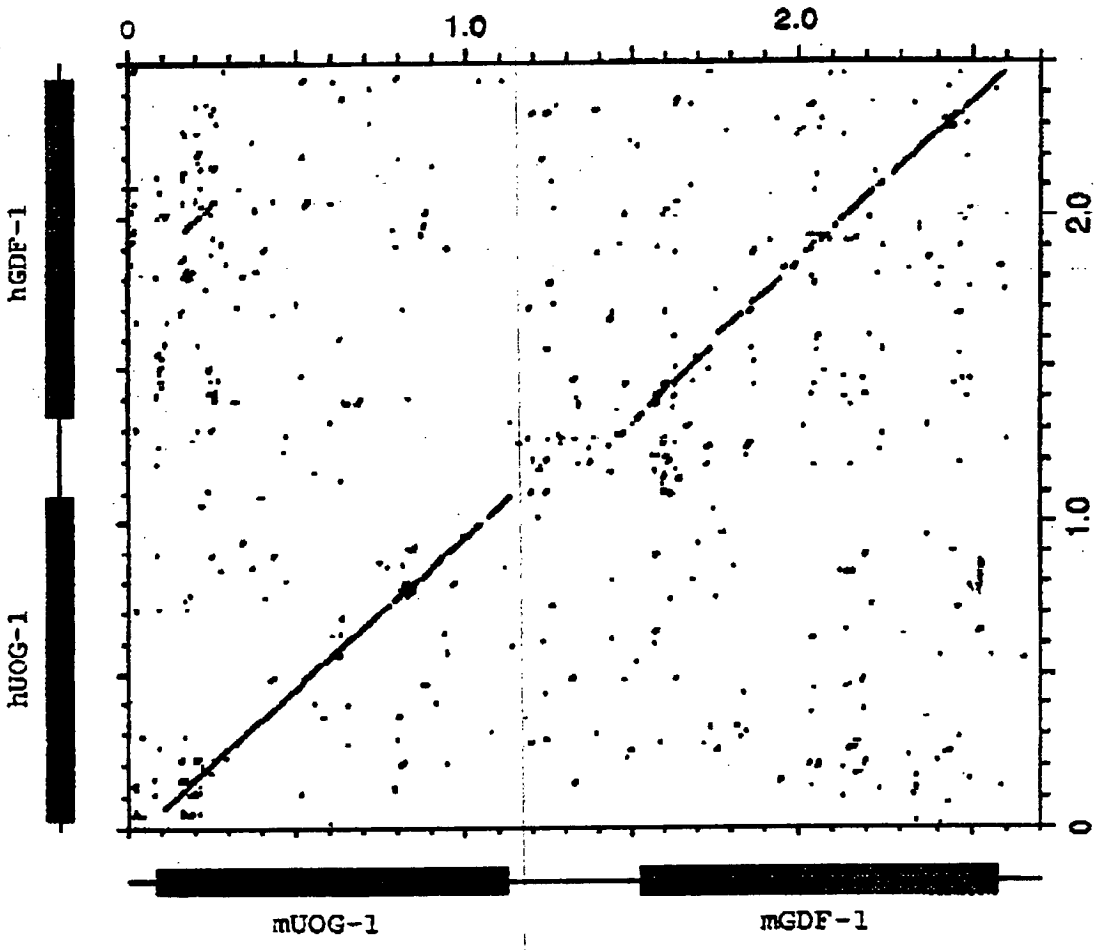

Fig 13c

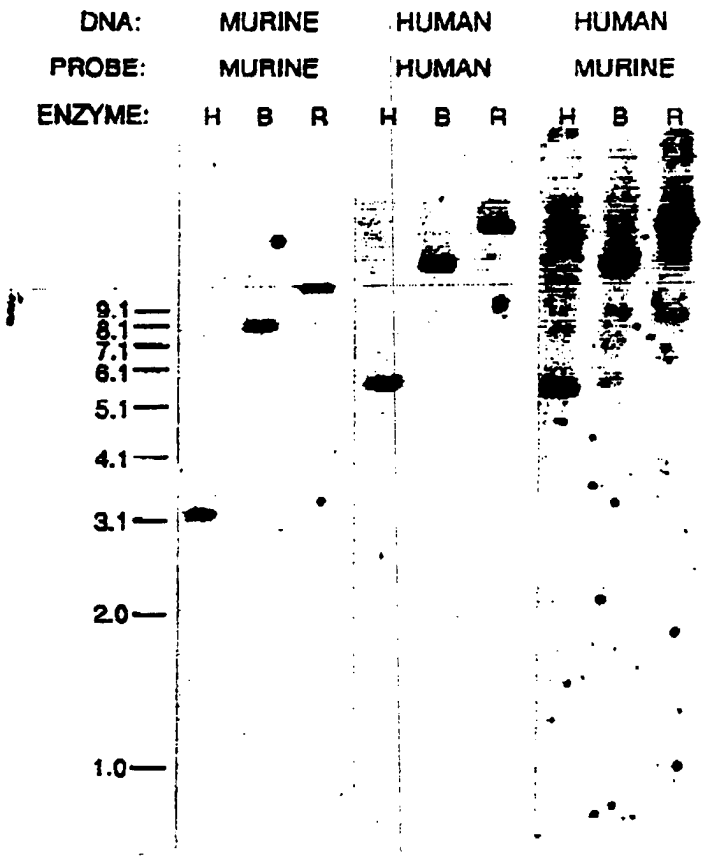
DNA:
MURINE
HUMAN
HUMAN
PROBE:
MURINE
HUMAN
MURINE
ENZYME:
H B R H B R H B R
9.1
8.1
7.1
6.1
5.1
4.1
3.1
2.0
1.0

Fig 14